GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 22, 2004, 16:31:15 ; Search time 8.44503 Seconds
(without alignments)
2650.131 Million cell updates/sec

Title: US-09-830-972-32
Perfect score: 705
Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	680.5	96.5	522	21	AAY71312	Rat neurite growth
2	510	72.3	199	23	ABB81077	Rat neurotransmitt
3	503	71.3	118	23	ABB89192	Human polypeptide
4	503	71.3	199	19	AAW53947	Human NSPLP protei
5	503	71.3	199	20	AAY35903	Extended human sec
6	503	71.3	199	20	AAW78313	Fragment of human
7	503	71.3	199	21	AAB12805	Human NSPH protein
8	503	71.3	199	22	AAB82348	Human NOGO-C prote
9	503	71.3	199	23	ABB81080	Human neurotransmi
10	503	71.3	199	23	ABG30939	Human NogoC protei
11	499.5	70.9	199	21	AAY71559	Rat Nogo C/Nogo A
12	448	63.5	1178	21	AAY71311	Human neurite grow
13	447	63.4	403	21	AAY71563	Rat Nogo A protein
14	447	63.4	893	21	AAY95012	Human secreted pro
15	447	63.4	983	24	ABU11573	Human MDDT polypep
16	447	63.4	1162	21	AAY71557	Rat Nogo A truncat
17	447	63.4	1163	21	AAY71310	Rat neurite growth
18	447	63.4	1163	21	AAY71384	Alternative versio
19	447	63.4	1163	23	ABB81074	Rat neurotransmitt
20	447	63.4	1192	21	AAY56967	Human MAGI polypep
21	447	63.4	1192	22	AAU04591	Human Nogo protein
22	447	63.4	1192	22	AAB82349	Human NOGO-A prote
23	447	63.4	1192	23	ABP68600	Human pancreatic c
24	447	63.4	1192	23	ABB81078	Human neurotransmi
25	447	63.4	1192	23	ABG30938	Human NogoA protei
26	443	62.8	103	22	AAE03980	Human gene 42 enco
27	443	62.8	200	22	AAB64514	Human secreted pro
28	443	62.8	359	21	AAY71558	Rat Nogo A protein
29	443	62.8	360	21	AAY71383	Rat neurite growth
30	443	62.8	360	22	AAE03987	Human gene 42 enco
31	443	62.8	360	23	ABB81076	Rat neurotransmitt
32	443	62.8	361	21	AAY71385	Alternative versio
33	443	62.8	373	21	AAB24242	Human Nogo B prote
34	443	62.8	373	21	AAY56969	Human MAGI polypep
35	443	62.8	373	21	AAY53624	A bone marrow secr
36	443	62.8	373	22	AAB82350	Human NOGO-B prote
37	443	62.8	373	23	ABP68601	Human pancreatic c
38	443	62.8	373	23	ABB81079	Human neurotransmi
39	443	62.8	373	23	ABG30937	Human NogoB protei
40	443	62.8	373	23	AAM47954	Human RTN4B SEQ ID
41	440	62.4	91	20	AAY12360	Human 5' EST secre
42	439	62.3	291	22	AAM93484	Human polypeptide,
43	410.5	58.2	642	19	AAW58383	Human secreted pro
44	410.5	58.2	642	22	AAB90682	Human BG160_1 prot
45	367	52.1	120	22	AAE03939	Human gene 42 enco

ALIGNMENTS

```
RESULT 1
AAY71312
ID   AAY71312 standard; Protein; 522 AA.
XX
AC   AAY71312;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat neurite growth inhibitor Nogo C.
XX
KW   Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          1..39
FT                   /note= "Sequence upstream to the N-terminus of
FT                   Nogo C protein"
FT   Protein         40..238
FT                   /label= Nogo_C_protein
FT   Region          11..191
FT                   /note= "Region specifically described in claim 16"
FT   Region          239..522
FT                   /note= "Sequence downstream to the C-terminus of
FT                   Nogo C protein"
FT   Region          51..238
FT                   /note= "C-terminal common region found in Nogo A, B
FT                   and C isoforms "
FT   Misc-difference 3
FT                   /note= "Encoded by TAG"
FT   Misc-difference 29
FT                   /note= "Encoded by TAA"
FT   Misc-difference 239
FT                   /note= "Encoded by TGA"
FT   Misc-difference 263
FT                   /note= "Encoded by TGA"
FT   Misc-difference 276
FT                   /note= "Encoded by TAG"
FT   Misc-difference 281
FT                   /note= "Encoded by TGA"
FT   Misc-difference 295
FT                   /note= "Encoded by TAA"
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FT   Misc-difference 314
FT                   /note= "Encoded by TGA"
FT   Misc-difference 318
FT                   /note= "Encoded by TGA"
FT   Misc-difference 335
FT                   /note= "Encoded by TAG"
FT   Misc-difference 371
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FT /note= "Encoded by TGA"
FT Misc-difference 374
FT /note= "Encoded by TAG"
FT Misc-difference 380
FT /note= "Encoded by TAA"
FT Misc-difference 406
FT /note= "Encoded by TAA"
FT Misc-difference 408
FT /note= "Encoded by TAG"
FT Misc-difference 410
FT /note= "Encoded by TAA"
FT Misc-difference 422
FT /note= "Encoded by TAA"
FT Misc-difference 433
FT /note= "Encoded by TGA"
FT Misc-difference 440
FT /note= "Encoded by TAG"
FT Misc-difference 453
FT /note= "Encoded by TAG"
FT Misc-difference 465
FT /note= "Encoded by TAG"
FT Misc-difference 482
FT /note= "Encoded by TAG"
FT Misc-difference 513
FT /note= "Encoded by TAA"
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US26160.
XX
PR 06-NOV-1998; 98US-0107446.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
DR N-PSDB; AAD01175.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic
PT disorders of the central nervous system and inducing regeneration of
PT neurons -
XX
PS Claim 7; Fig 14; 122pp; English.
XX
CC The present sequence is a rat Nogo C protein which is a
CC potent neural cell growth inhibitor and is free of all central nervous
CC system (CNS) myelin material with which it is natively associated.
CC Nogo proteins and fragments displaying neurite growth inhibitory
CC activity are used in the treatment of neoplastic disease of the CNS
CC e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve
CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which

CC promote Nogo activity can be used to treat or prevent hyperproliferative
CC or benign dysproliferative disorders e.g. psoriasis and tissue
CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
CC inhibit production of Nogo protein to induce regeneration of neurons or
CC to promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired.
CC The animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which
CC can treat or prevent disorders or diseases of the CNS.
CC Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29
CC in disclosure of the specification. However the specification does not
CC include sequences for these SEQ ID numbers.
XX
SQ Sequence 522 AA;

Query Match 96.5%; Score 680.5; DB 21; Length 522;
Best Local Similarity 98.6%; Pred. No. 1.3e-71;
Matches 138; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy          3 SGEAGVSCLRENFAVYSVSVGMHNL-LLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKT 61
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          4 SGEAGVSCLRENFAVYSVSVGMHNLXLLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKT 63

Qy         62 GVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSDEGHPFRAYL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db         64 GVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYL 123

Qy        122 ESEVAISEELVQKYSNSALG 141
              ||||||||||||||||||||
Db        124 ESEVAISEELVQKYSNSALG 143
```

RESULT 2
ABB81077
ID ABB81077 standard; Protein; 199 AA.
XX
AC ABB81077;
XX
DT 05-NOV-2002 (first entry)
XX
DE Rat neurotransmitter receptor protein Nogo-C.
XX
KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; rat; receptor.
XX
OS Rattus norvegicus.
XX
PN US2002072493-A1.
XX
PD 13-JUN-2002.
XX
PF 28-JUN-2001; 2001US-0893348.
XX

PR 19-MAY-1998; 98IL-0124500.
PR 21-JUL-1998; 98WO-US14715.
PR 22-DEC-1998; 98US-0218277.
PR 19-MAY-1999; 99US-0314161.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;
XX
DR WPI; 2002-607255/65.
DR N-PSDB; ABN86600.
XX
PT Promoting nerve regeneration and preventing neuronal degeneration in
PT the central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides -
XX
PS Example 5; Page 48-49; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease
CC is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents the rat
CC neurotransmitter receptor protein Nogo-C, an example of NS-specific
CC antigen.
XX
SQ Sequence 199 AA;

Query Match 72.3%; Score 510; DB 23; Length 199;
Best Local Similarity 99.0%; Pred. No. 5.3e-52;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97

```
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Db          1 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy         98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
                 |||||||||||  |||||||||||||||||||||||||||||||
Db         61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104


RESULT 3
ABB89192
ID   ABB89192 standard; Protein; 118 AA.
XX
AC   ABB89192;
XX
DT   24-MAY-2002  (first entry)
XX
DE   Human polypeptide SEQ ID NO 1568.
XX
KW   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW   antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW   vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW   cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; human; secreted protein.
XX
OS   Homo sapiens.
XX
PN   WO200190304-A2.
XX
PD   29-NOV-2001.
XX
PF   18-MAY-2001; 2001WO-US16450.
XX
PR   19-MAY-2000; 2000US-205515P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Birse CE,  Rosen CA;
XX
DR   WPI; 2002-122018/16.
DR   N-PSDB; ABL89601.
XX
PT   Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT   prevention of neural, immune system, muscular, reproductive,
PT   gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT   disorders -
XX
PS   Claim 11; SEQ ID NO 1568; 2081pp + Sequence Listing; English.
XX
CC   The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC   (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC   medical conditions e.g. by protein or gene therapy. The genes are
CC   isolated from a range of human tissues disclosed in the specification.
CC   The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC   in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC   and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC   marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC   (b) immune disorders e.g. Addison's disease, allergies, autoimmune
```

CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 118 AA;

Query Match 71.3%; Score 503; DB 23; Length 118;
Best Local Similarity 98.1%; Pred. No. 1.8e-51;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy         38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
              ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy         98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              |||||||||||  |||||||||||||||||||||||||||||||
Db         61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
```

RESULT 4
AAW53947
ID AAW53947 standard; Protein; 199 AA.
XX
AC AAW53947;
XX
DT 24-JUL-1998 (first entry)
XX
DE Human NSPLP protein A.
XX
KW NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;
KW neurodegenerative disease; amyotrophic lateral sclerosis; cancer.
XX
OS Homo sapiens.
XX
PN WO9806841-A2.
XX
PD 19-FEB-1998.
XX
PF 24-JUL-1997; 97WO-US13469.
XX
PR 12-AUG-1996; 96US-0700607.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Au-Young J, Bandman O, Goli SK, Hillman J;
XX
DR WPI; 1998-159533/14.
DR N-PSDB; AAV23695.
XX
PT Human neuro-endocrine-specific protein-like proteins - useful for
PT diagnosis, monitoring and treatment of cancer and neuro-degenerative

PT disease
XX
PS Claim 1; Page 38; 73pp; English.
XX
CC This sequence is a human neuroendocrine-specific protein-like
CC protein (NSPLP) of the invention. Recombinant cells transformed with the
CC DNA are used to express the NSPLP proteins, which are used to treat
CC cancer and neurodegenerative diseases such as amyotrophic lateral
CC sclerosis. Also antisense nucleic acids and antagonists of NSPLP can be
CC used to inhibit activity of the NSPLP proteins. Antibodies specific for
CC NSPLP are used for diagnosis and monitoring treatment of diseases
CC associated with NSPLP expression, in usual immunoassays, and to isolate
CC NSPLP from natural sources. The NSPLP proteins, or their fragments can
CC also be used in drug screening to identify NSPLP antagonists. The nucleic
CC acid can be used diagnostically and for monitoring treatment (in
CC hybridisation or amplification assays); to isolate closely related
CC sequences; in gene therapy for both sense and antisense applications
CC (including use of ribozymes) and for mapping the natural genomic
CC sequence.
XX
SQ Sequence 199 AA;

Query Match 71.3%; Score 503; DB 19; Length 199;
Best Local Similarity 98.1%; Pred. No. 3.6e-51;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy         38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
              ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy         98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              |||||||||||| |||||||||||||||||||||||||||||||
Db         61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
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RESULT 5
AAY35903
ID AAY35903 standard; Protein; 199 AA.
XX
AC AAY35903;
XX
DT 13-SEP-1999 (first entry)
XX
DE Extended human secreted protein sequence, SEQ ID NO. 152.
XX
KW Secreted protein; human; cytokine; cellular proliferation; cell movement;
KW cellular differentiation; immune system regulator; anti-inflammatory;
KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
KW genetic disease.
XX
OS Homo sapiens.
XX
PN WO9931236-A2.
XX
PD 24-JUN-1999.
XX

PF 17-DEC-1998; 98WO-IB02122.
XX
PR 10-AUG-1998; 98US-0096116.
PR 17-DEC-1997; 97US-0069957.
PR 09-FEB-1998; 98US-0074121.
PR 13-APR-1998; 98US-0081563.
XX
PA (GEST) GENSET.
XX
PI Bougueleret L, Duclert A, Dumas Milne Edwards J;
XX
DR WPI; 1999-385906/32.
DR N-PSDB; AAX97587.
XX
PT New isolated human secreted proteins
XX
PS Claim 9; Page 185-186; 516pp; English.
XX
CC This sequence is encoded by an extended human secreted protein coding
CC sequence of the invention. The secreted proteins can be used in treating
CC or controlling a variety of human conditions. The secreted proteins may
CC act as cytokines or may affect cellular proliferation or differentiation
CC or may act as immune system regulators, haematopoiesis regulators, tissue
CC growth regulators, regulators of reproductive hormones or cell movement
CC or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
CC tumour inhibition activity. The DNAs can be used in forensic procedures
CC to identify individuals or in diagnostic procedures to identify
CC individuals having genetic diseases resulting from abnormal expression of
CC the genes corresponding to the extended cDNAs. They are also useful for
CC constructing a high resolution map of the human chromosomes. They can
CC also be used for gene therapy to control or treat genetic diseases.
XX
SQ Sequence 199 AA;

  Query Match 71.3%; Score 503; DB 20; Length 199;
  Best Local Similarity 98.1%; Pred. No. 3.6e-51;
  Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy         98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              |||||||||||| |||||||||||||||||||||||||||||||
Db         61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
```

RESULT 6
AAW78313
ID AAW78313 standard; Protein; 199 AA.
XX
AC AAW78313;
XX
DT 13-APR-1999 (first entry)
XX
DE Fragment of human secreted protein encoded by gene 69.
XX

KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9856804-A1.
XX
PD 17-DEC-1998.
XX
PF 11-JUN-1998; 98WO-US12125.
XX
PR 02-OCT-1997; 97US-0061060.
PR 13-JUN-1997; 97US-0049547.
PR 13-JUN-1997; 97US-0049548.
PR 13-JUN-1997; 97US-0049549.
PR 13-JUN-1997; 97US-0049550.
PR 13-JUN-1997; 97US-0049606.
PR 13-JUN-1997; 97US-0049607.
PR 13-JUN-1997; 97US-0049608.
PR 13-JUN-1997; 97US-0049609.
PR 13-JUN-1997; 97US-0049610.
PR 13-JUN-1997; 97US-0049611.
PR 13-JUN-1997; 97US-0050566.
PR 13-JUN-1997; 97US-0050901.
PR 13-JUN-1997; 97US-0052989.
PR 08-JUL-1997; 97US-0051919.
PR 18-AUG-1997; 97US-0055984.
PR 12-SEP-1997; 97US-0058665.
PR 12-SEP-1997; 97US-0058668.
PR 12-SEP-1997; 97US-0058669.
PR 12-SEP-1997; 97US-0058750.
PR 12-SEP-1997; 97US-0058971.
PR 12-SEP-1997; 97US-0058972.
PR 12-SEP-1997; 97US-0058975.
PR 02-OCT-1997; 97US-0060834.
PR 02-OCT-1997; 97US-0060841.
PR 02-OCT-1997; 97US-0060844.
PR 02-OCT-1997; 97US-0060865.
PR 02-OCT-1997; 97US-0061059.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Brewer LA, Ebner R, Ferrie AM, Feng P, Greene JM, Lafleur DW;
PI Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
PI Yu GL;
XX
DR WPI; 1999-080881/07.
DR N-PSDB; AAX04379.
XX
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological

PT disorders, immune diseases, inflammation or blood disorders
XX
PS Disclosure; Page 62; 380pp; English.
XX
CC This sequence represents a fragment of a secreted human protein encoded
CC by the nucleic acid molecule detailed in the descriptor line. The gene
CC can be used to generate fusion proteins by linking to the gene to a
CC human immunoglobulin Fc portion (e.g. AAX04302) for increasing the
CC stability of the fused protein as compared to the human protein only.
CC The invention relates to 86 novel genes and their fragments (nucleic
CC acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 86
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAX04311 for described uses).
XX
SQ Sequence 199 AA;

Query Match 71.3%; Score 503; DB 20; Length 199;
Best Local Similarity 98.1%; Pred. No. 3.6e-51;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy         38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
              ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy         98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              |||||||||||| |||||||||||||||||||||||||||||||
Db         61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
```

RESULT 7
AAB12805
ID AAB12805 standard; Protein; 199 AA.
XX
AC AAB12805;
XX
DT 24-NOV-2000 (first entry)
XX
DE Human NSPH protein sequence SEQ ID NO:4.
XX
KW Human; neuroendocrine-specific protein; NSPH; NSPA; NSPB; NSPC.
XX
OS Homo sapiens.
XX
PN CN1253180-A.
XX
PD 17-MAY-2000.
XX
PF 30-OCT-1998; 98CN-0121473.
XX
PR 30-OCT-1998; 98CN-0121473.
XX
PA (UYFU-) UNIV FUDAN.

XX
PI Yu L, Zhao Y, Zhang H;
XX
DR WPI; 2000-466537/41.
DR N-PSDB; AAA72981.
XX
PT Specific protein of human neuroendocrine, coding sequence and its
PT preparating process and application -
XX
PS Claim 4; Page 14-15; 21pp; Chinese.
XX
CC The present invention relates to a new member of the human
CC neuroendocrine specific protein family, designated NSPH. The present
CC sequence represents the human NSPH protein.
XX
SQ Sequence 199 AA;

Query Match 71.3%; Score 503; DB 21; Length 199;
Best Local Similarity 98.1%; Pred. No. 3.6e-51;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy         38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
              ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy         98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              |||||||||||| |||||||||||||||||||||||||||||||
Db         61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
```

RESULT 8
AAB82348
ID AAB82348 standard; Protein; 199 AA.
XX
AC AAB82348;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human NOGO-C protein.
XX
KW NOGO-C; human; chromosome 2p21; neuropathy; spinal injury;
KW brain injury; stroke; neuronal degeneration; Alzheimer's disease;
KW Parkinson's disease; neuromuscular disorder; psychiatric disorder;
KW developmental disorder; neuroprotective; nootropic; neuroleptic;
KW antiparkinsonian; cerebroprotective; neuroleptic; diagnosis;
KW therapy.
XX
OS Homo sapiens.
XX
PN WO200136631-A1.
XX
PD 25-MAY-2001.
XX
PF 14-NOV-2000; 2000WO-GB04345.
XX
PR 15-NOV-1999; 99GB-0026995.
PR 24-JAN-2000; 2000GB-0001550.

XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Michalovich D, Prinjha R;
XX
DR WPI; 2001-343822/36.
DR N-PSDB; AAF90323.
XX
PT New polypeptide designated NOGO-C is a splice variant of the human NOGO
PT gene and may be useful in the treatment of neural disorders including
PT Alzheimer's and Parkinson's diseases -
XX
PS Claim 3; Page 25; 25pp; English.
XX
CC The present sequence is that of human NOGO-C, encoded by a novel
CC splice variant of the human NOGO gene on chromosome 2p21. 2 Other
CC splice variants, NOGO-A and NOGO-B, have previously been identified.
CC The invention provides NOGO-C polypeptides and polynucleotides, and
CC methods for producing such polypeptides by recombinant techniques.
CC Also disclosed are methods for utilising NOGO-C polypeptides and
CC polynucleotides in the treatment of diseases including neuropathies,
CC spinal injury, brain injury, stroke, neuronal degeneration, for
CC example Alzheimer's disease and Parkinson's disease, neuromuscular
CC disorders, psychiatric disorders and developmental disorders. Also
CC provided are methods for identifying agonists and agonists for
CC use in treating conditions associated with NOGO-C imbalance, and
CC diagnostic assays for detecting diseases associated with
CC inappropriate NOGO-C activity or levels.
XX
SQ Sequence 199 AA;

Query Match 71.3%; Score 503; DB 22; Length 199;
Best Local Similarity 98.1%; Pred. No. 3.6e-51;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy         38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
              ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy         98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              |||||||||||| |||||||||||||||||||||||||||||||
Db         61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
```

RESULT 9
ABB81080
ID ABB81080 standard; Protein; 199 AA.
XX
AC ABB81080;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human neurotransmitter receptor protein Nogo-C.
XX
KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;

KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; human; receptor.
XX
OS Homo sapiens.
XX
PN US2002072493-A1.
XX
PD 13-JUN-2002.
XX
PF 28-JUN-2001; 2001US-0893348.
XX
PR 19-MAY-1998; 98IL-0124500.
PR 21-JUL-1998; 98WO-US14715.
PR 22-DEC-1998; 98US-0218277.
PR 19-MAY-1999; 99US-0314161.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;
XX
DR WPI; 2002-607255/65.
DR N-PSDB; ABN86601.
XX
PT Promoting nerve regeneration and preventing neuronal degeneration in
PT the central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides -
XX
PS Examples; Page 57-58; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease
CC is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,

CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents the human
CC neurotransmitter receptor protein Nogo-C, an example of NS-specific
CC antigen.
XX
SQ Sequence 199 AA;

Query Match 71.3%; Score 503; DB 23; Length 199;
Best Local Similarity 98.1%; Pred. No. 3.6e-51;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy         38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
              |||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy         98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              |||||||||||| |||||||||||||||||||||||||||||||
Db         61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
```

RESULT 10
ABG30939
ID ABG30939 standard; Protein; 199 AA.
XX
AC ABG30939;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human NogoC protein.
XX
KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
KW tissue hypertrophy; central nervous system; axon regeneration; NogoC;
KW Nogo-associated disease; metastasis.
XX
OS Homo sapiens.
XX
PN WO200257483-A2.
XX
PD 25-JUL-2002.
XX
PF 18-JAN-2002; 2002WO-GB00228.
XX
PR 18-JAN-2001; 2001GB-0001312.
XX
PA (GLAX) GLAXO GROUP LTD.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Blackstock WP, Hale RS, Prinjha R, Rowley A;
XX
DR WPI; 2002-599722/64.
DR N-PSDB; ABK90135.
XX
PT Identifying modulators of Nogo or BACE activity for treating acute
PT neuronal injuries, neoplastic or dysproliferative disorders, comprises

PT providing and monitoring interaction between Nogo and BACE polypeptides
PT -
XX
PS Disclosure; Page 64; 68pp; English.
XX
CC The present invention relates to a new method of identifying modulators
CC of Nogo function or BACE activity. The method involves providing Nogo and
CC BACE polypeptides capable of binding with each other, monitoring the
CC interaction between these polypeptides, and determining if the test agent
CC is a modulator of Nogo or BACE activity. The method is useful in treating
CC acute neuronal injuries, such as spinal or head injury, stroke,
CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,
CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.
CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue
CC hypertrophy) of the central nervous system. The BACE polypeptide is
CC useful in screening methods to identify agents that may act as modulators
CC of BACE activity and in particular agents that may be useful in treating
CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,
CC and the polynucleotide encoding the BACE polypeptide are useful in
CC manufacturing a medicament for the treatment or prevention of disorders
CC responsive to the modulation of Nogo activity, in alleviating the
CC symptoms or improving the condition of a patient suffering from this
CC disorder, in axon regeneration, or in preventing metastasis or spreading
CC of a cancer. The polynucleotide may also be an essential component in
CC assays, a probe, in recombinant protein synthesis, and in gene therapy
CC techniques. The present amino acid sequence represents the human NogoC
CC protein of the invention.
XX
SQ Sequence 199 AA;

Query Match 71.3%; Score 503; DB 23; Length 199;
Best Local Similarity 98.1%; Pred. No. 3.6e-51;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy         38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
              ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy         98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              |||||||||||| |||||||||||||||||||||||||||||||
Db         61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104
```

RESULT 11
AAY71559
ID AAY71559 standard; Protein; 199 AA.
XX
AC AAY71559;
XX
DT 02-NOV-2000 (first entry)
XX
DE Rat Nogo C/Nogo A proteins derived fragment to construct mutant Nogo-C.
XX
KW Rat; neurite growth inhibitor; Nogo A; Nogo C; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Region 1..11
FT /note= "Corresponds to residues 40-50 of rat Nogo C
FT protein shown in AAY71312"
FT Region 12..199
FT /note= "Corresponds to residues 975-1162 of rat Nogo A
FT protein shown in AAY71310"
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US26160.
XX
PR 06-NOV-1998; 98US-0107446.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic
PT disorders of the central nervous system and inducing regeneration of
PT neurons -
XX
PS Example; Page -; 122pp; English.
XX
CC The patent relates to neurite growth inhibitor Nogo which is free of
CC all central nervous system (CNS) myelin material with which it is
CC natively associated. Nogo proteins and fragments displaying neurite
CC growth inhibitory activity are used in the treatment of neoplastic
CC disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
CC craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
CC neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma
CC and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
CC diseases. Therapeutics which promote Nogo activity can be used to treat
CC or prevent hyperproliferative or benign dysproliferative disorders e.g.
CC psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic
CC acids can be used to inhibit production of Nogo protein to induce
CC regeneration of neurons or to promote structural plasticity of the CNS
CC in disorders where neurite growth, regeneration or maintenance are
CC deficient or desired. The animal models can be used in diagnostic and
CC screening methods for predisposition to disorders and to screen for or
CC test molecules which can treat or prevent disorders or diseases of the
CC CNS. The present sequence is derived by fusing two fragments from rat
CC Nogo C and Nogo A proteins. The fragment is used in the construction of
CC mutant Nogo-C which is composed of
CC His-tag/T7-tag/Nogo-C N-terminus (11 aa) + Nogo-A sequence aa 975-1162.
CC Nogo A deletion mutants were used for mapping the inhibitory sites of

```
CC   Nogo protein. Major inhibitory region was identified in the
CC   Nogo A sequence from amino acids 172-974, particularly amino acids
CC   542-722. In addition, N-terminal region 1-171 was found to be inhibitory
CC   to NIH 3T3 fibroblast spreading.
CC   Note: The present sequence is not given in the specification but is
CC   derived from rat Nogo C sequence shown in AAY71312 and Nogo A sequence
CC   shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and
CC   SEQ ID NO: 29 in disclosure of the specification. However, the
CC   specification does not include sequences for these SEQ ID numbers.
XX
SQ   Sequence   199 AA;

  Query Match             70.9%;  Score 499.5;  DB 21;  Length 199;
  Best Local Similarity   98.1%;  Pred. No. 9.3e-51;
  Matches  103;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         38 MDGQKKHWKDK-VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTI 96
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDGQKKHWKDKSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTI 60

Qy         97 SFRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              |||||||||||| |||||||||||||||||||||||||||||||
Db         61 SFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 105


RESULT 12
AAY71311
ID   AAY71311 standard; Protein; 1178 AA.
XX
AC   AAY71311;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Human neurite growth inhibitor Nogo.
XX
KW   Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 187
FT                   /label= Unknown
FT   Misc-difference 188
FT                   /label= Unknown
FT   Misc-difference 189
FT                   /label= Unknown
FT   Misc-difference 190
FT                   /label= Unknown
FT   Misc-difference 221
FT                   /label= Unknown
FT   Misc-difference 328
```

FT /label= Unknown
FT Misc-difference 477
FT /label= Unknown
FT Region 994..1174
FT /note= "Region specifically described in claim 16"
FT Region 977..1012
FT /note= "Region specifically described in claim 16"
FT Region 1079..1114
FT /note= "Region specifically described in claim 16"
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US26160.
XX
PR 06-NOV-1998; 98US-0107446.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic
PT disorders of the central nervous system and inducing regeneration of
PT neurons -
XX
PS Claim 11; Fig 13; 122pp; English.
XX
CC The present sequence is a human Nogo protein which is a
CC potent neural cell growth inhibitor and is free of all central nervous
CC system (CNS) myelin material with which it is natively associated. The
CC human Nogo sequence was derived by aligning human expressed sequence tags
CC (ESTs) e.g. AA158636, AA333267, AA081783, AA167765, AA322918, AA092565,
CC AA081525 and AA081840 with the rat Nogo sequence.
CC Nogo proteins and fragments displaying neurite growth inhibitory
CC activity are used in the treatment of neoplastic disease of the CNS
CC e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve
CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
CC promote Nogo activity can be used to treat or prevent hyperproliferative
CC or benign dysproliferative disorders e.g. psoriasis and tissue
CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
CC inhibit production of Nogo protein to induce regeneration of neurons or
CC to promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired.
CC The animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which
CC can treat or prevent disorders or diseases of the CNS.
CC Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29
CC in disclosure of the specification. However the specification does not
CC include sequences for these SEQ ID numbers.
XX
SQ Sequence 1178 AA;

```
  Query Match             63.5%;  Score 448;  DB 21;  Length 1178;
  Best Local Similarity   74.6%;  Pred. No. 1.3e-43;
  Matches   97;  Conservative    3;  Mismatches    8;  Indels   22;  Gaps    1;

Qy         12 RENFAVYSVSVGMHNLLLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFL 71
              |   |::|  :|                      |  ||||||||||||||||||||||
Db        976 RSPSAIFSADLG--------------------KTSVVDLLYWRDIKKTGVVFGASLFL 1013

Qy         72 LLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSDEGHPFRAYLESEVAISEEL 131
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1014 LLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEEL 1073

Qy        132 VQKYSNSALG 141
              ||||||||||
Db       1074 VQKYSNSALG 1083


RESULT 13
AAY71563
ID   AAY71563 standard; Protein; 403 AA.
XX
AC   AAY71563;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat Nogo A protein fragment used in the construction of mutant EST.
XX
KW   Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening; mutant; mutein.
XX
OS   Rattus sp.
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;   99WO-US26160.
XX
PR   06-NOV-1998;   98US-0107446.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic
PT   disorders of the central nervous system and inducing regeneration of
PT   neurons -
XX
```

PS Example; Page -; 122pp; English.
XX
CC The patent relates to neurite growth inhibitor Nogo which is free of
CC all central nervous system (CNS) myelin material with which it is
CC natively associated. Nogo proteins and fragments displaying neurite
CC growth inhibitory activity are used in the treatment of neoplastic
CC disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
CC craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
CC neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma
CC and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
CC diseases. Therapeutics which promote Nogo activity can be used to treat
CC or prevent hyperproliferative or benign dysproliferative disorders e.g.
CC psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic
CC acids can be used to inhibh ction of Nogo protein100; induce
CC regeneration of neurons or to promote structural plasticity of the CNS
CC in disorders where neurite growth, regeneration or maintenance are
CC deficient or desired. The animal models can be used in diagnostic and
CC screening methods for predisposition to disorders and to screen for or
CC test molecules which can treat or prevent disorders or diseases of the
CC CNS. The present sequence is a fragment of rat Nogo A protein shown in
CC AAY71310, which is used in the construction of mutant EST. The mutant
CC is composed of His-tag/T7-tag/Nogo-A sequence aa 760-1162.
CC Nogo A deletion mutants were used for mapping the inhibitory sites of
CC Nogo protein. Major inhibitory region was identified in the
CC Nogo A sequence from amino acids 172-974, particularly amino acids
CC 542-722. In addition, N-terminal region 1-171 was found to be inhibitory
CC to NIH 3T3 fibroblast spreading.
CC Note: The present sequence is not given in the specification but is
CC derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42
CC are referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However, the specification does not include sequences for
CC these SEQ ID numbers.
XX
SQ Sequence 403 AA;

Query Match 63.4%; Score 447; DB 21; Length 403;
Best Local Similarity 96.9%; Pred. No. 3.9e-44;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
               |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         214 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 273

Qy         106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
               ||| |||||||||||||||||||||||||||||||
Db         274 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 309
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RESULT 14
AAY95012
ID AAY95012 standard; Protein; 893 AA.
XX
AC AAY95012;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human secreted protein vb22_1, SEQ ID NO:64.

XX

KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW neurodegenerative disease; asthma; contraceptive.

XX

OS Homo sapiens.

XX

PN WO200011015-A1.

XX

PD 02-MAR-2000.

XX

PF 24-AUG-1999; 99WO-US19351.

XX

PR 24-AUG-1998; 98US-0097638.
PR 24-AUG-1998; 98US-0097659.
PR 09-SEP-1998; 98US-0099618.
PR 28-SEP-1998; 98US-0102092.
PR 25-NOV-1998; 98US-0109978.
PR 23-DEC-1998; 98US-0113645.
PR 23-DEC-1998; 98US-0113646.
PR 23-AUG-1999; 99US-0379246.

XX

PA (ALPH-) ALPHAGENE INC.

XX

PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

XX

DR WPI; 2000-224657/19.

XX

PT New secreted or transmembrane proteins and polynucleotides encoding
PT them, useful for treating neurodegenerative disorders, autoimmune
PT diseases and cancer -

XX

PS Claim 73; Page 322-325; 357pp; English.

XX

CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted
CC proteins of the invention include those that are thought to be only
CC partially secreted, i.e., transmembrane proteins. The proteins of the
CC invention may exhibit one or more activities selected from the following:
CC cytokine activity; cell proliferation; differentiation; immune
CC modulation; haematopoiesis regulation; tissue growth activity;
CC activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic
CC and thrombolytic activity; anti-inflammatory activity; and tumour
CC inhibition activity. The proteins may be administered to patients as
CC vaccines, and the nucleotides may be used as part of a gene therapy
CC regime. Diseases or conditions that may be treated using the proteins or
CC nucleotides of the invention include autoimmune diseases; genetic
CC disorders; haemophilia; cardiovascular diseases; cancer; bacterial,
CC fungal and viral infections, especially HIV; multiple sclerosis;
CC rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;
CC insulin dependent diabetes mellitus; and allergic reactions such as
CC asthma and anaemia. They may also be used for treating wounds, burns,
CC ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease and amyotrophic
CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may
CC additionally be useful as contraceptives. Nucleic acid sequences of the

```
CC   invention may be used in chromosome mapping, and as a source of
CC   diagnostic primers and probes. The present sequence represents one of the
CC   40 proteins of the invention.
XX
SQ   Sequence   893 AA;

  Query Match             63.4%;  Score 447;  DB 21;  Length 893;
  Best Local Similarity   96.9%;  Pred. No. 1.1e-43;
  Matches   93;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
              |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        703 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 762

Qy        106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              ||| ||||||||||||||||||||||||||||||||
Db        763 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 798


RESULT 15
ABU11573
ID   ABU11573 standard; Protein; 983 AA.
XX
AC   ABU11573;
XX
DT   12-FEB-2003  (first entry)
XX
DE   Human MDDT polypeptide SEQ ID 520.
XX
KW   MDDT; human; disease detection and treatment molecule polypeptide;
KW   anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
KW   haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
KW   gene therapy; protein replacement therapy; cell proliferative disorder;
KW   cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
KW   anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW   Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
KW   psoriasis; hepatitis.
XX
OS   Homo sapiens.
XX
PN   WO200279449-A2.
XX
PD   10-OCT-2002.
XX
PF   27-MAR-2002; 2002WO-US09944.
XX
PR   28-MAR-2001; 2001US-279619P.
PR   29-MAR-2001; 2001US-280067P.
PR   29-MAR-2001; 2001US-280068P.
PR   16-MAY-2001; 2001US-291280P.
PR   17-MAY-2001; 2001US-291829P.
PR   17-MAY-2001; 2001US-291849P.
PR   19-JUN-2001; 2001US-299428P.
PR   20-JUN-2001; 2001US-299776P.
PR   20-JUN-2001; 2001US-300001P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
```

XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-058431/05.
DR N-PSDB; ABX34563.
XX
PT New purified disease detection and treatment molecule proteins and
PT polynucleotides, useful for diagnosing, treating or preventing cancers
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT or hepatitis -
XX
PS Claim 27; SEQ ID NO 520; 339pp + Sequence Listing; English.
XX
CC This invention describes a novel disease detection and treatment molecule
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
CC and the polypeptides of the invention can be used for gene therapy,
CC protein replacement therapy and are useful for treating a variety of
CC diseases or conditions. These polypeptides or polynucleotides are
CC particularly useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded
CC by ABU11450-ABU11845, described in the disclosure of the invention.
CC NOTE: The sequence data for this p d not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 983 AA;

Query Match 63.4%; Score 447; DB 24; Length 983;
Best Local Similarity 96.9%; Pred. No. 1.3e-43;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
               |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         793 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 852

Qy         106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
               ||| |||||||||||||||||||||||||||||||
Db         853 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 888
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Search completed: January 22, 2004, 16:36:41
Job time : 13.445 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 22, 2004, 16:31:15 ; Search time 3.42077 Seconds
(without alignments)
1744.001 Million cell updates/sec

Title: US-09-830-972-32
Perfect score: 705
Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	503	71.3	199	2	US-08-700-607-1	Sequence 1, Appli
2	349	49.5	208	2	US-08-700-607-7	Sequence 7, Appli
3	348	49.4	267	2	US-08-700-607-8	Sequence 8, Appli
4	337	47.8	356	2	US-08-700-607-6	Sequence 6, Appli
5	337	47.8	776	2	US-08-700-607-5	Sequence 5, Appli
6	305	43.3	241	2	US-08-700-607-3	Sequence 3, Appli
7	227	32.2	168	4	US-09-149-476-563	Sequence 563, App
8	99	14.0	80	3	US-08-905-223-411	Sequence 411, App
9	75	10.6	593	4	US-09-328-352-4866	Sequence 4866, Ap
10	72.5	10.3	598	2	US-08-853-659A-53	Sequence 53, Appl
11	71.5	10.1	154	1	US-08-366-783-5	Sequence 5, Appli

12	70	9.9	518	4	US-09-134-001C-4744	Sequence 4744, Ap
13	70	9.9	563	4	US-09-422-936-79	Sequence 79, Appl
14	70	9.9	619	3	US-08-262-220-6	Sequence 6, Appli
15	70	9.9	619	3	US-08-471-733-6	Sequence 6, Appli
16	70	9.9	619	3	US-08-468-878-6	Sequence 6, Appli
17	70	9.9	619	3	US-08-750-494-6	Sequence 6, Appli
18	70	9.9	619	4	US-08-470-638-6	Sequence 6, Appli
19	70	9.9	844	4	US-09-422-936-47	Sequence 47, Appl
20	70	9.9	844	4	US-09-422-936-51	Sequence 51, Appl
21	70	9.9	886	4	US-09-422-936-77	Sequence 77, Appl
22	70	9.9	892	4	US-09-422-936-75	Sequence 75, Appl
23	70	9.9	899	4	US-09-422-936-71	Sequence 71, Appl
24	70	9.9	960	4	US-09-422-936-45	Sequence 45, Appl
25	70	9.9	961	4	US-09-422-936-49	Sequence 49, Appl
26	70	9.9	961	4	US-09-914-259-14	Sequence 14, Appl
27	69	9.8	621	3	US-08-262-220-8	Sequence 8, Appli
28	69	9.8	621	3	US-08-471-733-8	Sequence 8, Appli
29	69	9.8	621	3	US-08-468-878-8	Sequence 8, Appli
30	69	9.8	621	3	US-08-750-494-8	Sequence 8, Appli
31	69	9.8	621	4	US-08-470-638-8	Sequence 8, Appli
32	68	9.6	344	4	US-09-107-532A-6886	Sequence 6886, Ap
33	68	9.6	1447	3	US-09-041-886-25	Sequence 25, Appl
34	68	9.6	1447	5	PCT-US94-05277-2	Sequence 2, Appli
35	67.5	9.6	659	4	US-09-328-352-6021	Sequence 6021, Ap
36	67	9.5	231	4	US-09-198-452A-419	Sequence 419, App
37	67	9.5	507	4	US-09-328-352-7742	Sequence 7742, Ap
38	66.5	9.4	249	4	US-09-107-532A-6706	Sequence 6706, Ap
39	66	9.4	445	4	US-09-328-352-4714	Sequence 4714, Ap
40	65.5	9.3	187	2	US-08-846-021A-5	Sequence 5, Appli
41	65.5	9.3	234	1	US-08-366-783-4	Sequence 4, Appli
42	65.5	9.3	254	2	US-08-767-026-7	Sequence 7, Appli
43	65.5	9.3	254	4	US-09-319-275A-7	Sequence 7, Appli
44	65	9.2	964	4	US-09-422-936-53	Sequence 53, Appl
45	64.5	9.1	614	1	US-08-291-299-7	Sequence 7, Appli

ALIGNMENTS

```
RESULT 1
US-08-700-607-1
; Sequence 1, Application US/08700607
; Patent No. 5858708
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Hillman, Jennifer L.
;    TITLE OF INVENTION:  TWO NOVEL HUMAN NSP-LIKE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
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;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/700,607
;       FILING DATE:  Filed Herewith
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J.
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0114 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  199 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:
;       CLONE:  Consensus
US-08-700-607-1

  Query Match             71.3%;  Score 503;  DB 2;  Length 199;
  Best Local Similarity   98.1%;  Pred. No. 2.3e-52;
  Matches  102;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
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Db          1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy         98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              |||||||||||  |||||||||||||||||||||||||||||||
Db         61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104


RESULT 2
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Hillman, Jennifer L.
;    TITLE OF INVENTION:  TWO NOVEL HUMAN NSP-LIKE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
```

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;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/700,607
;       FILING DATE:  Filed Herewith
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J.
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0114 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  208 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:  GenBank
;       CLONE:  307311
US-08-700-607-7

  Query Match             49.5%;  Score 349;  DB 2;  Length 208;
  Best Local Similarity   63.4%;  Pred. No. 7e-34;
  Matches   64;  Conservative   19;  Mismatches   18;  Indels    0;  Gaps    0;

Qy         37 EMDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTI 96
              :||    :|| : :|||||||||:||:|||: | || ||| ||:||| ||:||| || ||
Db          9 KMDCVWSNWKSQAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATI 68

Qy         97 SFRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
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Db         69 SFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEQIQKYTD 109


RESULT 3
US-08-700-607-8
; Sequence 8, Application US/08700607
; Patent No. 5858708
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Hillman, Jennifer L.
;    TITLE OF INVENTION:  TWO NOVEL HUMAN NSP-LIKE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
```

```
;       COUNTRY:  U.S.
;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/700,607
;       FILING DATE:  Filed Herewith
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J.
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0114 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  267 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:  GenBank
;       CLONE:  281046
US-08-700-607-8

  Query Match             49.4%;  Score 348;  DB 2;  Length 267;
  Best Local Similarity   64.0%;  Pred. No. 1.3e-33;
  Matches   64;  Conservative   18;  Mismatches   18;  Indels    0;  Gaps    0;

Qy         38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
              ||    :|| : :||||||||||:||:|||: | || ||| ||:||| ||:||| || |||
Db          1 MDCVWSNWKSQAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATIS 60

Qy         98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
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Db         61 FRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEQIQKYTD 100


RESULT 4
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Hillman, Jennifer L.
;    TITLE OF INVENTION:  TWO NOVEL HUMAN NSP-LIKE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
```

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;       STATE:  CA
;       COUNTRY:  U.S.
;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/700,607
;       FILING DATE:  Filed Herewith
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J.
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0114 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  356 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:  GenBank
;       CLONE:  307309
US-08-700-607-6

  Query Match             47.8%;  Score 337;  DB 2;  Length 356;
  Best Local Similarity   67.4%;  Pred. No. 4e-32;
  Matches   62;  Conservative   16;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
               | | :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:
Db         166 KQKAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVL 225

Qy         106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
               ||: |:||||||:|||| |: :|:| :|||::
Db         226 QAVQKTDEGHPFKAYLELEITLSQEQIQKYTD 257


RESULT 5
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Hillman, Jennifer L.
;    TITLE OF INVENTION:  TWO NOVEL HUMAN NSP-LIKE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
```

```
;       CITY:  Palo Alto
;       STATE:  CA
;       COUNTRY:  U.S.
;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/700,607
;       FILING DATE:  Filed Herewith
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J.
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0114 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  776 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:  GenBank
;       CLONE:  307307
US-08-700-607-5

  Query Match             47.8%;  Score 337;  DB 2;  Length 776;
  Best Local Similarity   67.4%;  Pred. No. 1.2e-31;
  Matches   62;  Conservative   16;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
               | | :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:
Db         586 KQKAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVL 645

Qy         106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
               ||: |:||||||:|||| |: :|:| :|||::
Db         646 QAVQKTDEGHPFKAYLELEITLSQEQIQKYTD 677


RESULT 6
US-08-700-607-3
; Sequence 3, Application US/08700607
; Patent No. 5858708
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Hillman, Jennifer L.
;    TITLE OF INVENTION:  TWO NOVEL HUMAN NSP-LIKE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
```

```
;       STREET:  3174 Porter Drive
;       CITY:  Palo Alto
;       STATE:  CA
;       COUNTRY:  U.S.
;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/700,607
;       FILING DATE:  Filed Herewith
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J.
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0114 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  241 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:  THP1NOB01
;       CLONE:  31870
US-08-700-607-3

  Query Match             43.3%;  Score 305;  DB 2;  Length 241;
  Best Local Similarity   60.9%;  Pred. No. 1.6e-28;
  Matches   56;  Conservative   17;  Mismatches   19;  Indels    0;  Gaps    0;

Qy         49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108
              | ||: |||:|||| ||| :| :|||| ||::|| :|: |||||||||||||| ||||:
Db         48 VHDLIXWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQAV 107

Qy        109 AKSDEGHPFRAYLESEVAISEELVQKYSNSAL 140
               ||:|||||:|||: :: :| |    | |:|:
Db        108 QKSEEGHPFKAYLDVDITLSSEAFHNYMNAAM 139


RESULT 7
US-09-149-476-563
; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P1
;  CURRENT APPLICATION NUMBER: US/09/149,476
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: PCT/US98/04493
;  EARLIER FILING DATE: 1998-03-06
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; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601

```
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC       block the regeneration of the nervous central system in adults (By
CC       similarity).
CC   -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
CC       membrane of the endoplasmic reticulum through 2 putative
CC       transmembrane domains (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=1;
CC         Comment=A number of isoforms may be produced;
CC       Name=1;
CC         IsoId=Q99P72-1; Sequence=Displayed;
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF326337; AAK08076.1; -.
DR   EMBL; AK003859; -; NOT_ANNOTATED_CDS.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0030176; C:endoplasmic reticulum membrane, intrinsic p. . .; ISS.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0005635; C:nuclear membrane; ISS.
DR   GO; GO:0005515; F:protein binding activity; ISS.
DR   GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR   GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT   DOMAIN        1     25       CYTOPLASMIC (Potential).
FT   TRANSMEM     26     50       POTENTIAL.
```

```
FT   DOMAIN       51    137       LUMENAL (Potential).
FT   TRANSMEM    138    162       POTENTIAL.
FT   DOMAIN      163    199       CYTOPLASMIC (Potential).
FT   DOMAIN       12    199       RETICULON.
SQ   SEQUENCE   199 AA;  22466 MW;  07BE5D580059ED9C CRC64;

  Query Match             70.2%;  Score 495;  DB 1;  Length 199;
  Best Local Similarity   97.1%;  Pred. No. 1.8e-41;
  Matches  101;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 97
              || ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDDQKKRWKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy         98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              |||||||||||| ||||||||||||||||||||||||||||||
Db         61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104


RESULT 2
RTN4_RAT
ID   RTN4_RAT       STANDARD;      PRT;  1163 AA.
AC   Q9JK11; Q9JK10; Q9R0D9; Q9WUE9; Q9WUF0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
DE   (Glut4 vesicle 20 kDa protein).
GN   RTN4 OR NOGO.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
RX   MEDLINE=99249816; PubMed=10231557;
RA   Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
RT   "Cloning and characterization of a 22 kDa protein from rat adipocytes:
RT   a new member of the reticulon family.";
RL   Biochim. Biophys. Acta 1450:68-76(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX   MEDLINE=20129258; PubMed=10667796;
RA   Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
RA   Spillmann A.A., Christ F., Schwab M.E.;
RT   "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
RT   antigen for monoclonal antibody IN-1.";
RL   Nature 403:434-439(2000).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
RC   STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
RA   Ito T., Schwartz S.M.;
RT   "Cloning of a member of the reticulon gene family in rat: one of two
RT   minor splice variants.";
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
```

```
RP   FUNCTION.
RX   MEDLINE=22033691; PubMed=12037567;
RA   GrandPre T., Li S., Strittmatter S.M.;
RT   "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
RL   Nature 417:547-551(2002).
CC   -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC       block the regeneration of the nervous central system in adults (By
CC       similarity).
CC   -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
CC       membrane of the endoplasmic reticulum through 2 putative
CC       transmembrane domains (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1; Synonyms=Nogo-A, NI-220-250;
CC         IsoId=Q9JK11-1; Sequence=Displayed;
CC       Name=2; Synonyms=Nogo-B, Foocen-M1;
CC         IsoId=Q9JK11-2; Sequence=VSP_005658;
CC       Name=3; Synonyms=Nogo-C, VP20;
CC         IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;
CC       Name=4; Synonyms=Foocen-M2;
CC         IsoId=Q9JK11-4; Sequence=VSP_005659;
CC   -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
CC       nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
CC       present in dorsal root ganglion, sciatic nerve and PC12 cells
CC       after longer exposure. Isoforms 2 and 3 are detected in kidney,
CC       cartilage, skin, lung and spleen. Isoform 3 is expressed at high
CC       level in skeletal muscle. In adult animals isoform 1 is expressed
CC       mainly in the nervous system.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF051335; AAF01564.1; -.
DR   EMBL; AJ242961; CAB71027.1; -.
DR   EMBL; AJ242962; CAB71028.1; -.
DR   EMBL; AJ242963; CAB71029.1; -.
DR   EMBL; AF132045; AAD31019.1; -.
DR   EMBL; AF132046; AAD31020.1; -.
DR   GO; GO:0030176; C:endoplasmic reticulum membrane, intrinsic p. . .; IDA.
DR   GO; GO:0005635; C:nuclear membrane; ISS.
DR   GO; GO:0005515; F:protein binding activity; ISS.
DR   GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR   GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT   DOMAIN        1    989       CYTOPLASMIC (Potential).
FT   TRANSMEM    990   1010       POTENTIAL.
```

```
FT   DOMAIN      1011   1104       LUMENAL (Potential).
FT   TRANSMEM    1105   1125       POTENTIAL.
FT   DOMAIN      1126   1163       CYTOPLASMIC (Potential).
FT   DOMAIN       976   1163       RETICULON.
FT   DOMAIN        33     46       POLY-GLU.
FT   DOMAIN        73     76       POLY-ALA.
FT   DOMAIN       140    145       POLY-PRO.
FT   VARSPLIC       1    964       Missing (in isoform 3).
FT                                 /FTId=VSP_005656.
FT   VARSPLIC     965    975       AVLSAELSKTS -> MDGQKKHWKDK (in isoform
FT                                 3).
FT                                 /FTId=VSP_005657.
FT   VARSPLIC     173    975       Missing (in isoform 2).
FT                                 /FTId=VSP_005658.
FT   VARSPLIC     192    975       Missing (in isoform 4).
FT                                 /FTId=VSP_005659.
FT   CONFLICT    1130   1131       MISSING (IN REF. 3; AAD31020).
SQ   SEQUENCE    1163 AA;  126386 MW;  8CB894B09E94F0B6 CRC64;

  Query Match             63.4%;  Score 447;  DB 1;  Length 1163;
  Best Local Similarity   96.9%;  Pred. No. 6.1e-36;
  Matches   93;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
              |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1032

Qy        106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              ||| |||||||||||||||||||||||||||||||||
Db       1033 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1068


RESULT 3
RTN4_HUMAN
ID   RTN4_HUMAN     STANDARD;      PRT;  1192 AA.
AC   Q9NQC3; O94962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;
AC   Q9Y5U6;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
DE   (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific
DE   protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
GN   RTN4 OR NOGO OR ASY OR KIAA0886.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX   MEDLINE=20129242; PubMed=10667780;
RA   Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,
RA   Michalovich D., Simmons D.L., Walsh F.S.;
RT   "Inhibitor of neurite outgrowth in humans.";
RL   Nature 403:383-384(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
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RC TISSUE=Brain;
RX MEDLINE=21010696; PubMed=11126360;
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
RT endoplasmic reticulum and reduces their anti-apoptotic activity.";
RL Oncogene 19:5736-5746(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20237542; PubMed=10773680;
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
RT 2p14-->2p13 by radiation hybrid mapping.";
RL Cytogenet. Cell Genet. 88:101-102(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RA Jin W.-L., Ju G.;
RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Placenta, and Skeletal muscle;
RA Ito T., Schwartz S.M.;
RT "Cloning of a member of the reticulon gene family in human.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fibroblast;
RA Yutsudo M.;
RT "Isolation of a cell death-inducing gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Pituitary;
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
RA Luo B., Hu R., Chen J.;
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel human cDNA clone with function of inhibiting cancer cell
RT growth.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
RN [10]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).

RC TISSUE=Brain, Pancreas, Placenta, and Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [11]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=20499367; PubMed=11042152;
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells.";
RL Genome Res. 10:1546-1560(2000).
RN [12]
RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
RC TISSUE=Brain;
RA Mao Y.M., Xie Y., Zheng Z.H.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN [13]
RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RA Sha J.H., Zhou Z.M., Li J.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN [14]
RP TOPOLOGY.
RC TISSUE=Brain;
RX MEDLINE=20129259; PubMed=10667797;
RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;
RT "Identification of the Nogo inhibitor of axon regeneration as a
RT Reticulon protein.";
RL Nature 403:439-444(2000).
RN [15]
RP FUNCTION.
RC TISSUE=Brain;
RX MEDLINE=21069055; PubMed=11201742;
RA Fournier A.E., Grandpre T., Strittmatter S.M.;
RT "Identification of a receptor mediating Nogo-66 inhibition of axonal
RT regeneration.";

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RL   Nature 409:341-346(2001).
RN   [16]
RP   REVIEW.
RX   MEDLINE=21888956; PubMed=11891768;
RA   Ng C.E.L., Tang B.L.;
RT   "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
RT   regeneration.";
RL   J. Neurosci. Res. 67:559-565(2002).
CC   -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC       block the regeneration of the nervous central system in adults.
CC       Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.
CC       This is likely consecutive to their change in subcellular
CC       location, from the mitochondria to the endoplasmic reticulum,
CC       after binding and sequestration.
CC   -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC       reticulum. Anchored to the membrane of the endoplasmic reticulum
CC       through 2 putative transmembrane domains.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;
CC         IsoId=Q9NQC3-1; Sequence=Displayed;
CC       Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;
CC         IsoId=Q9NQC3-2; Sequence=VSP_005655;
CC       Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
CC         IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
CC       Name=4;
CC         IsoId=Q9NQC3-4; Sequence=VSP_005654;
CC   -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
CC       and testis and weakly in heart and skeletal muscle. Isoform 2 is
CC       widely expressed excepted for the liver. Isoform 3 is expressed in
CC       brain, skeletal muscle and adipocytes. Isoform 4 is testis-
CC       specific.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   -!- CAUTION: Ref.11 sequence differs from that shown due to
CC       frameshifts in positions 1149 and 1156.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ251383; CAB99248.1; -.
DR   EMBL; AJ251384; CAB99249.1; -.
DR   EMBL; AJ251385; CAB99250.1; -.
DR   EMBL; AB040462; BAB18927.1; -.
DR   EMBL; AB040463; BAB18928.1; -.
DR   EMBL; AF148537; AAG12176.1; -.
DR   EMBL; AF148538; AAG12177.1; -.
DR   EMBL; AF087901; AAG12205.1; -.
DR   EMBL; AF320999; AAG40878.1; -.
DR   EMBL; AF132047; AAD31021.1; -.
DR   EMBL; AF132048; AAD31022.1; -.
DR   EMBL; AB015639; BAA83712.1; -.
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DR   EMBL; AF077050; AAD27783.1; -.
DR   EMBL; AF177332; AAG17976.1; -.
DR   EMBL; AB020693; BAA74909.1; -.
DR   EMBL; BC001035; AAH01035.1; -.
DR   EMBL; BC007109; AAH07109.1; -.
DR   EMBL; BC014366; AAH14366.1; -.

  Query Match           63.4%;  Score 447;  DB 1;  Length 1192;
  Best Local Similarity  96.9%;  Pred. No. 6.2e-36;
  Matches   93;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
              |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1002 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1061

Qy        106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
              ||| |||||||||||||||||||||||||||||||||
Db       1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097


RESULT 4
RTN1_HUMAN
ID   RTN1_HUMAN     STANDARD;      PRT;   776 AA.
AC   Q16799; Q16800; Q16801;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Reticulon 1 (Neuroendocrine-specific protein).
GN   RTN1 OR NSP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS RTN1-A; RTN1-B AND RTN1-C).
RC   TISSUE=Lung carcinoma;
RX   MEDLINE=93293865; PubMed=7685762;
RA   Roebroek A.J.M., Van de Velde H.J.K., Van Bokhoven A., Broers J.L.V.,
RA   Ramaekers F.C.S., Van de Ven W.J.M.;
RT   "Cloning and expression of alternative transcripts of a novel
RT   neuroendocrine-specific gene and identification of its 135-kDa
RT   translational product.";
RL   J. Biol. Chem. 268:13439-13447(1993).
RN   [2]
RP   ALTERNATIVE SPLICING.
RX   MEDLINE=96429995; PubMed=8833145;
RA   Roebroek A.J.M., Ayoubi T.A.Y., Van de Velde H.J.K.,
RA   Schoenmakers E.F.P.M., Pauli I.G.L., Van de Ven W.J.M.;
RT   "Genomic organization of the human NSP gene, prototype of a novel gene
RT   family encoding reticulons.";
RL   Genomics 32:191-199(1996).
RN   [3]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=98228245; PubMed=9560466;
RA   Hens J., Nuydens R., Geerts H., Senden N.H., Van de Ven W.J.M.,
RA   Roebroek A.J., van de Velde H.J., Ramaekers F.C., Broers J.L.;
RT   "Neuronal differentiation is accompanied by NSP-C expression.";
```

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RL   Cell Tissue Res. 292:229-237(1998).
CC   -!- FUNCTION: MAY BE INVOLVED IN NEUROENDOCRINE SECRETION OR IN
CC       MEMBRANE TRAFFICKING IN NEUROENDOCRINE CELLS.
CC   -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=RTN1-A; Synonyms=NSP-A;
CC         IsoId=Q16799-1; Sequence=Displayed;
CC       Name=RTN1-B; Synonyms=NSP-B;
CC         IsoId=Q16799-2; Sequence=VSP_005644;
CC       Name=RTN1-C; Synonyms=NSP-C;
CC         IsoId=Q16799-3; Sequence=VSP_005645, VSP_005646;
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES
CC       AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C
CC       IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.
CC   -!- PTM: ISOFORMS RTN1-A AND RTN1-C ARE PHOSPHORYLATED.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L10333; AAA59950.1; -.
DR   EMBL; L10334; AAA59951.1; -.
DR   EMBL; L10335; AAA59952.1; -.
DR   PIR; A46583; A46583.
DR   PIR;   0904; I609p4475X
DR   Genew; HGNC:10467; RTN1.
DR   MIM; 600865; -.
DR   GO; GO:0030176; C:endoplasmic reticulum membrane, intrinsic p. . .; TAS.
DR   GO; GO:0004871; F:signal transducer activity; NAS.
DR   GO; GO:0030182; P:neuron differentiation; TAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane;
KW   Phosphorylation.
FT   TRANSMEM    603    623       POTENTIAL.
FT   TRANSMEM    726    746       POTENTIAL.
FT   DOMAIN      589    776       RETICULON.
FT   DOMAIN      609    612       POLY-LEU.
FT   VARSPLIC      1    420       Missing (in isoform RTN1-B).
FT                                /FTId=VSP_005644.
FT   VARSPLIC      1    568       Missing (in isoform RTN1-C).
FT                                /FTId=VSP_005645.
FT   VARSPLIC    569    588       GPGPLGPGAPPPLLFLNKQK -> MQATADSTKMDCVWSNW
FT                                KSQ (in isoform RTN1-C).
FT                                /FTId=VSP_005646.
SQ   SEQUENCE   776 AA;  83617 MW;  CA5B6232353096FE CRC64;

  Query Match             47.8%;  Score 337;  DB 1;  Length 776;
  Best Local Similarity   67.4%;  Pred. No. 2.4e-25;
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  Matches   62;  Conservative   16;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
               | | :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:
Db         586 KQKAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVL 645

Qy         106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
               ||: |:||||||:|||| |: :|:| :|||::
Db         646 QAVQKTDEGHPFKAYLELEITLSQEQIQKYTD 677


RESULT 5
RTN1_RAT
ID   RTN1_RAT       STANDARD;      PRT;   777 AA.
AC   Q64548; Q64547;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Reticulon 1 (Neuroendocrine-specific protein) (S-rex).
GN   RTN1 OR NSP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS RTN1-B AND RTN1-S).
RC   STRAIN=Wistar; TISSUE=Brain cortex;
RX   MEDLINE=96386034; PubMed=8793864;
RA   Baka I.D., Ninkina N.N., Pinon L.G.P., Adu J., Davies A.M.,
RA   Georgiev G.P., Buchman V.L.;
RT   "Intracellular compartmentalization of two differentially spliced s-
RT   rex/NSP mRNAs in neurons.";
RL   Mol. Cell. Neurosci. 7:289-303(1996).
CC   -!- FUNCTION: MAY BE INVOLVED IN NEUROENDOCRINE SECRETION OR IN
CC       MEMBRANE TRAFFICKING IN NEUROENDOCRINE CELLS.
CC   -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM MEMBRANE (BY
CC       SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=RTN1-B; Synonyms=S-RexB;
CC         IsoId=Q64548-1; Sequence=Displayed;
CC       Name=RTN1-S; Synonyms=S-RexS;
CC         IsoId=Q64548-2; Sequence=VSP_005647, VSP_005648;
CC   -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND
CC       PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS
CC       HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.
CC       EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL
CC       TYPES.
CC   -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE
CC       HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC
CC       DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN
CC       THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXB
CC       DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE
CC       HINDBRAIN.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; U17604; AAC53046.1; -.
DR   EMBL; U17603; AAC53045.1; -.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT   TRANSMEM    604    624       POTENTIAL.
FT   TRANSMEM    727    747       POTENTIAL.
FT   DOMAIN      590    777       RETICULON.
FT   DOMAIN      610    613       POLY-LEU.
FT   VARSPLIC      1    569       Missing (in isoform RTN1-S).
FT                               /FTId=VSP_005647.
FT   VARSPLIC    570    589       IPGPLGSDLVPPLPFFNKQK -> MQATADSTKMDCVWSNW
FT                               KSQ (in isoform RTN1-S).
FT                               /FTId=VSP_005648.
SQ   SEQUENCE   777 AA;  83001 MW;  AF7479C50F28D0AC CRC64;

  Query Match             47.8%;  Score 337;  DB 1;  Length 777;
  Best Local Similarity   67.4%;  Pred. No. 2.4e-25;
  Matches   62;  Conservative   16;  Mismatches   14;  Indels    0;  Gaps    0;

Qy         46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
              | | :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:
Db        587 KQKAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVL 646

Qy        106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
              ||: |:||||||:|||| |: :|:| :|||::
Db        647 QAVQKTDEGHPFKAYLELEITLSQEQIQKYTD 678


RESULT 6
RTN3_HUMAN
ID   RTN3_HUMAN     STANDARD;      PRT;   236 AA.
AC   O95197;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like
DE   protein II) (NSPLII).
GN   RTN3 OR NSPL2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC   TISSUE=Retina;
RX   MEDLINE=99265974; PubMed=10331947;
RA   Moreira E.F., Jaworski C.J., Rodriguez I.R.;
RT   "Cloning of a novel member of the reticulon gene family (RTN3): gene
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RT   structure and chromosomal localization to 11q13.";
RL   Genomics 58:73-81(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Huang X., Zhou Y., Du G., Yuan J., Qiang B.;
RT   "Cloning and expression analysis of a cDNA encoding a novel
RT   neuroendocrine-specific protein-like protein 1: NSPL1.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, Eye, and Lymph;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC       reticulum (Potential).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN
CC       BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL
CC       RETINA.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF059524; AAC99319.1; -.
DR   EMBL; AF059529; AAD20951.1; -.
DR   EMBL; AF059525; AAD20951.1; JOINED.
DR   EMBL; AF059526; AAD20951.1; JOINED.
DR   EMBL; AF059527; AAD20951.1; JOINED.
DR   EMBL; AF059528; AAD20951.1; JOINED.
DR   EMBL; AF119297; AAD26810.1; -.
DR   EMBL; BC000634; AAH00634.1; -.
DR   EMBL; BC010556; AAH10556.1; -.
DR   EMBL; BC011394; AAH11394.1; -.
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DR   EMBL; BC022993; AAH22993.1; -.
DR   Genew; HGNC:10469; RTN3.
DR   MIM; 604249; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Transmembrane; Endoplasmic reticulum.
FT   TRANSMEM     68     88       POTENTIAL.
FT   TRANSMEM    177    197       POTENTIAL.
FT   DOMAIN       48    236       RETICULON.
SQ   SEQUENCE   236 AA;  25609 MW;  DDC6A4544ABCDFB7 CRC64;

  Query Match             43.8%;  Score 309;  DB 1;  Length 236;
  Best Local Similarity   60.9%;  Pred. No. 3.7e-23;
  Matches   56;  Conservative   18;  Mismatches   18;  Indels    0;  Gaps    0;

Qy         49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108
              | ||::|||:|||| ||| :| :|||| ||::|| :|: |||||||||||||| ||||:
Db         48 VHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQAV 107

Qy        109 AKSDEGHPFRAYLESEVAISEELVQKYSNSAL 140
               ||:|||||:|||: :: :| |    | |:|:
Db        108 QKSEEGHPFKAYLDVDITLSSEAFHNYMNAAM 139


RESULT 7
RTN3_MOUSE
ID   RTN3_MOUSE     STANDARD;      PRT;   237 AA.
AC   Q9ES97;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Reticulon protein 3.
GN   RTN3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Huang X., Zhou Y., Qiang H., Yuan J., Qiang B.;
RT   "Cloning and expression profile of a novel mouse cDNA encoding a human
RT   RTN3 homolog.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!  SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC       reticulum (Potential).
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
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DR   EMBL; AF195940; AAG31360.1; -.
DR   MGD; MGI:1339970; Rtn3.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Transmembrane; Endoplasmic reticulum.
FT   TRANSMEM     69     89       POTENTIAL.
FT   TRANSMEM    167    187       POTENTIAL.
FT   DOMAIN       49    237       RETICULON.
SQ   SEQUENCE   237 AA;  25428 MW;  EB60A0A7AC45F0DE CRC64;

  Query Match             43.7%;  Score 308;  DB 1;  Length 237;
  Best Local Similarity   59.8%;  Pred. No. 4.6e-23;
  Matches   55;  Conservative   19;  Mismatches   18;  Indels    0;  Gaps    0;

Qy         49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108
              | ||::|||:|||| ||| :| :|||| ||::|| :|: ||||||||||:|| ||||:
Db         49 VHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRVYKSVIQAV 108

Qy        109 AKSDEGHPFRAYLESEVAISEELVQKYSNSAL 140
               ||:|||||:|||: :: :| |    | |:|:
Db        109 QKSEEGHPFKAYLDVDITLSSEAFHNYMNAAM 140


RESULT 8
RTN2_HUMAN
ID   RTN2_HUMAN     STANDARD;      PRT;   545 AA.
AC   O75298; O60509;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like
DE   protein 1) (NSPLI).
GN   RTN2 OR NSPL1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RC   TISSUE=Lung carcinoma;
RX   MEDLINE=98360096; PubMed=9693037;
RA   Roebroek A.J.M., Contreras B., Pauli I.G.L., Van de Ven W.J.M.;
RT   "cDNA cloning, genomic organization, and expression of the human RTN2
RT   gene, a member of a gene family encoding reticulons.";
RL   Genomics 51:98-106(1998).
RN   [2]
RP   SEQUENCE OF 108-545 FROM N.A. (ISOFORM RTN2-B).
RC   TISSUE=Brain;
RX   MEDLINE=98191726; PubMed=9530622;
RA   Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
RT   "Molecular cloning of a novel mouse gene with predominant muscle and
RT   neural expression.";
RL   Mamm. Genome 9:274-282(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC       reticulum (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
```

```
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=RTN2-A;
CC         IsoId=O75298-1; Sequence=Displayed;
CC         Note=Isoform RTN2-C is produced by alternative initiation at
CC         Met-341 of isoform RTN2-A;
CC       Name=RTN2-B;
CC         IsoId=O75298-2; Sequence=VSP_005649;
CC       Event=Alternative initiation;
CC         Comment=2 isoforms, RTN2-A (shown here) and RTN2-C, are produced
CC         by alternative initiation at Met-1 and Met-341;
CC   -!- TISSUE SPECIFICITY: ISOFORM RTN2-C IS HIGHLY EXPRESSED IN SKELETAL
CC       MUSCLE.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF004222; AAC32542.1; -.
DR   EMBL; AF004223; AAC32543.1; -.
DR   EMBL; AF004224; AAC32544.1; -.
DR   EMBL; AF038540; AAC14910.1; -.
DR   Genew; HGNC:10468; RTN2.
DR   MIM; 603183; -.
DR   GO; GO:0030176; C:endoplasmic reticulum membrane, intrinsic p. . .; NAS.
DR   GO; GO:0004871; F:signal transducer activity; NAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane;
KW   Alternative initiation.
FT   CHAIN         1    545       RETICULON PROTEIN 2, ISOFORM RTN2-A.
FT   CHAIN       341    545       RETICULON PROTEIN 2, ISOFORM RTN2-C.
FT   INIT_MET    341    341       FOR ISOFORM RTN2-C.
FT   TRANSMEM    368    388       POTENTIAL.
FT   TRANSMEM    463    483       POTENTIAL.
FT   DOMAIN      345    545       RETICULON.
FT   VARSPLIC    272    344       Missing (in isoform RTN2-B).
FT                                /FTId=VSP_005649.
SQ   SEQUENCE   545 AA;  59263 MW;  971FD2F909E1E9E6 CRC64;

  Query Match             30.4%;  Score 214;  DB 1;  Length 545;
  Best Local Similarity   46.7%;  Pred. No. 1.8e-13;
  Matches   42;  Conservative   21;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         48 KVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 107
              || |||||:| : :|||    :  || |  |||||| |::|| ||  ||| |:|: |:||
Db        344 KVADLLYWKDTRTSGVVFTGLMVSLLCLLHFSIVSVAAHLALLLLCGTISLRVYRKVLQA 403

Qy        108 IAKSDEGHPFRAYLESEVAISEELVQKYSN 137
              : : |  :||:|||: :: :: |  :: |:
Db        404 VHRGDGANPFQAYLDVDLTLTREQTERLSH 433
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RESULT 9
RTN2_MOUSE
ID   RTN2_MOUSE     STANDARD;      PRT;   471 AA.
AC   O70622; O70620;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like
DE   protein 1) (NSPLI).
GN   RTN2 OR NSPL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
RC   STRAIN=FVB/N, and 129/Sv; TISSUE=Cerebellum, and Skeletal muscle;
RX   MEDLINE=98191726; PubMed=9530622;
RA   Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
RT   "Molecular cloning of a novel mouse gene with predominant b       d
RT   neural expression.";
RL   Mamm. Genome 9:274-282(1998).
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
CC       (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Brain;
CC         IsoId=O70622-1; Sequence=Displayed;
CC       Name=2; Synonyms=Muscle;
CC         IsoId=O70622-2; Sequence=VSP_005650, VSP_005651;
CC   -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN NEURAL AND MUSCULAR
CC       TISSUES.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF038537; AAC14906.1; -.
DR   EMBL; AF038537; AAC14907.1; -.
DR   EMBL; AF038538; AAC14908.1; -.
DR   EMBL; AF038539; AAC14909.1; -.
DR   EMBL; AF093624; AAD13195.1; -.
DR   MGD; MGI:107612; Rtn2.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT   TRANSMEM    295    315       POTENTIAL.
FT   DOMAIN      272    471       RETICULON.
FT5  VARSPLIC      1    267       Missing (in isoform 2).
```

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FT                                   /FTId=VSP_005650.
FT   VARSPLIC    268    271          PLLL -> MGSK (in isoform 2).
FT                                   /FTId=VSP_005651.
SQ   SEQUENCE   471 AA;  51346 MW;  9BBD8F372CF63AD3 CRC64;

  Query Match             27.9%;  Score 197;  DB 1;  Length 471;
  Best Local Similarity   44.3%;  Pred. No. 7.2e-12;
  Matches   39;  Conservative   20;  Mismatches   29;  Indels    0;  Gaps    0;

Qy         49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108
              | |||||:| : :| ||   :  || |  |||||| |::||  |  ||| |:|: |:||:
Db        272 VADLLYWKDTRTSGAVFTGLMASLLCLLHFSIVSVAAHLALLGLCATISLRVYRKVLQAV 331

Qy        109 AKSDEGHPFRAYLESEVAISEELVQKYS 136
               : |  :||:|||: :: :: |  :: |
Db        332 HRGDGTNPFQAYLDMDLTLTREQTERLS 359


RESULT 10
T2RD_MOUSE
ID   T2RD_MOUSE     STANDARD;      PRT;   243 AA.9
AC   Q9JKA2;
DT   15-SEP-2003 (Rel. 42, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Taste receptor type 2 member 13 (T2R13) (Taste receptor family B
DE   member 3) (TRB3) (Fragment).
GN   TAS2R13.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DBA/2J;
RX   MEDLINE=20227309; PubMed=10766242;
RA   Matsunami H., Montmayeur J.-P., Buck L.B.;
RT   "A family of candidate taste receptors in human and mouse.";
RL   Nature 404:601-604(2000).
RN   [2]
RP   REVIEW.
RX   MEDLINE=22135574; PubMed=12139982;
RA   Montmayeur J.-P., Matsunami H.;
RT   "Receptors for bitter and sweet taste.";
RL   Curr. Opin. Neurobiol. 12:366-371(2002).
RN                                                    CRC64
RP   REVIEW.
RX   MEDLINE=21634924; PubMed=11696554;
RA   Margolskee R.F.;
RT   "Molecular mechanisms of bitter and sweet taste transduction.";
RL   J. Biol. Chem. 277:1-4(2002).
RN   [4]
RP   REVIEW.
RX   MEDLINE=22469025; PubMed=12581520;
RA   Zhang Y., Hoon M.A., Chandrashekar J., Mueller K.L., Cook B., Wu D.,
RA   Zuker C.S., Ryba N.J.;
RT   "Coding of sweet, bitter, and umami tastes: different receptor cells
```

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RT   sharing similar signaling pathways.";
RL   Cell 112:293-301(2003).
CC   -!- FUNCTION: Receptor that may play a role in the perception of
CC       bitterness and is gustducin-linked. May play a role in sensing the
CC       chemical composition of the gastrointestinal content. The activity
CC       of this receptor may stimulate alpha gustducin, mediate PLC-beta-2
CC       activation and lead to the gating of TRPM5.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells
CC       of the tongue and palate epithelium and exclusively in gustducin-
CC       positive cells.
CC   -!- MISCELLANEOUS: Most taste cells may be activated by a limited
CC       number of bitter compounds; individual taste cells can
CC       discriminate among bitter stimuli.
CC   -!- SIMILARITY: Belongs to family T2R of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF247733; AAF64510.1; -.
DR   MGD; MGI:1890148; Tas2r13.
DR   Pfam; PF05296; TAS2R; 1.
KW   Receptor; G-protein coupled receptor; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN       <1     12       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     13     33       2 (POTENTIAL).
FT   DOMAIN       34     54       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     55     75       3 (POTENTIAL).
FT   DOMAIN       76     99       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    100    120       4 (POTENTIAL).
FT   DOMAIN      121    150       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    151    171       5 (POTENTIAL).
FT   DOMAIN      172    195       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    196    216       6 (POTENTIAL).
FT   DOMAIN      217    222       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    223   >243       7 (POTENTIAL).
FT   CARBOHYD    128    128       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   NON_TER     243    243
SQ   SEQUENCE   243 AA;  28110 MW;  D8AD14AF95B9E0B2 CRC64;

  Query Match             11.0%;  Score 77.5;  DB 1;  Length 243;
  Best Local Si           27.1%;  Pred. No. 1.8;
  Matches   32;  Conservative   18;  Mismatches   47;  Indels   21;  Gaps    5;

Qy         17 VYSVSVGMHNLLLLEGRSWQEMDGQKKH---WKDKVVDLLYWRDIKKTGVVFGASLFLLL 73
              :||  :    :|::   ||  ::    |   |    : : |:  |      |  |:|| |
Db         37 LYSALMTTRKVLIIFNNSWTVIN----HFNIWLATCLSIFYFLKIAN----FSNSIFLSL 88

Qy         74 SLTVFSIVSVTAYIALALLSV---------TISFRIYKGVIQAIAKSDEG-HPFRAYL 121
                | ::||||  ::| || |          ||  :||      : ||   |  | :|
Db         89 RWRVKTVVSVTLMMSLLLLFVNVLVINTFIVISVDVYKVNTSYSSHSDNNLHISRIFL 146
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RESULT 11
PHSC_ECOLI
ID   PHSC_ECOLI     STANDARD;      PRT;   261 AA.
AC   P77409;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   PhsC protein homolog.
GN   YDHU OR B1670.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RT   01B
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97175536; PubMed=9023191;
RA   Hensel M., Shea J.E., Baeumler A.J., Gleeson C., Blattner F.R.,
RA   Holden D.W.;
RT   "Analysis of the boundaries of Salmonella pathogenicity island 2 and
RT   the corresponding chromosomal region of Escherichia coli K-12.";
RL   J. Bacteriol. 179:1105-1111(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=97251357; PubMed=9097039;
RA   Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA   Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
RA   Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
RA   Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
RA   Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
RA   Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
RA   Yamamoto Y., Horiuchi T.;
RT   "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT   corresponding to the 28.0-40.1 min region on the linkage map.";
RL   DNA Res. 3:363-377(1996).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC       (Potential).
CC   -!- SIMILARITY: TO S.TYPHIMURIUM PHSC.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; AE000262; AAC74740.1; -.
DR   EMBL; U68703; AAB47946.1; -.
DR   EMBL; D90810; BAA15442.1; -.
DR   PIR; F64924; F64924.
DR   EcoGene; EG13955; ydhU.
DR   InterPro; IPR000516; Ni_hydr_CytB.
DR   Pfam; PF01292; Ni_hydr_CYTB; 1.
KW   Transmembrane; Inner membrane; Complete proteome.
FT   TRANSMEM     25     45       POTENTIAL.
FT   TRANSMEM     81    101       POTENTIAL.
FT   TRANSMEM    108    128       POTENTIAL.
FT   TRANSMEM    182    202       POTENTIAL.
FT   TRANSMEM    224    244       POTENTIAL.
SQ   SEQUENCE   261 AA;  29583 MW;  65CF1A45691A0AF3 CRC64;

  Query Match             11.0%;  Score 77.5;  DB 1;  Length 261;
  Best Local Similarity   27.6%;  Pred. No. 1.9;
  Matches   29;  Conservative   16;  Mismatches   48;  Indels        Gaps    4;

Qy         22 VGMHNLLLLEGRSWQEMD-GQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLL----SLT 76
              :|:| ||   |      | |:| :   | | | :| :         | ||:||     :
Db         44 LGLHALLRARGVKKSATDHGEKIYLYSKAVRLWHWSN---------ALLFVLLLASGLIN 94

Qy         77 VFSIVSVTAYIALALLSVTISFRI---YKGVIQAIAKSDEGHPFR 118
               |::|  ||  :|  :     | :   : | :   |  | || :|
Db         95 HFAMVGATAVKSLVAVHEVCGFLLLACWLGFVLINAVGDNGHHYR 139


RESULT 12
T2R8_MOUSE
ID   T2R8_MOUSE     STANDARD;      PRT;   246 AA.
AC   Q9JKA0;
DT   15-SEP-2003 (Rel. 42, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Taste receptor type 2 member 8 (T2R8) (Taste receptor family B member
DE   5) (TRB5) (Fragment).
GN   TAS2R8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mamma  a; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=20227309; PubMed=10766242;
RA   Matsunami H., Montmayeur J.-P., Buck L.B.;
RT   "A family of candidate taste receptors in human and mouse.";
RL   Nature 404:601-604(2000).
RN   [2]
RP   REVIEW.
RX   MEDLINE=22135574; PubMed=12139982;
RA   Montmayeur J.-P., Matsunami H.;
RT   "Receptors for bitter and sweet taste.";
RL   Curr. Opin. Neurobiol. 12:366-371(2002).
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RN   [3]
RP   REVIEW.
RX   MEDLINE=21634924; PubMed=11696554;
RA   Margolskee R.F.;
RT   "Molecular mechanisms of bitter and sweet taste transduction.";
RL   J. Biol. Chem. 277:1-4(2002).
RN   [4]
RP   REVIEW.
RX   MEDLINE=22469025; PubMed=12581520;
RA   Zhang Y., Hoon M.A., Chandrashekar J., Mueller K.L., Cook B., Wu D.,
RA   Zuker C.S., Ryba N.J.;
RT   "Coding of sweet, bitter, and umami tastes: different receptor cells
RT   sharing similar signaling pathways.";
RL   Cell 112:293-301(2003).
CC   -!- FUNCTION: Receptor that may play a role in the perception of
CC       bitterness and is gustducin-linked. May play a role in sensing the
CC       chemical composition of the gastrointestinal content. The activity
CC       of this receptor may stimulate alpha gustducin, mediate PLC-beta-2
CC       activation and lead to the gating of TRPM5.
CC   -!-              LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells
CC       of the tongue and palate epithelium and exclusively in gustducin-
CC       positive cells. Expressed in 15% taste bud cells in circumvallate
CC       and foliate papillae but only in 2% in fungiform papillae.
CC   -!- MISCELLANEOUS: Most taste cells may be activated by a limited
CC       number of bitter compounds; individual taste cells can
CC       discriminate among bitter stimuli.
CC   -!- SIMILARITY: Belongs to family T2R of G-protein coupled receptors.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF247735; AAF64512.1; -.
DR   MGD; MGI:1890259; Tas2r8.
DR   Pfam; PF05296; TAS2R; 1.
KW   Receptor; G-protein coupled receptor; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN        1     15       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     16     36       2 (POTENTIAL).
FT   DOMAIN       37     59       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     60     80       3 (POTENTIAL).
FT   DOMAIN       81    102       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    103    123       4 (POTENTIAL).
FT   DOMAIN      M N.A.456XN      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    154    174       5 (POTENTIAL).
FT   DOMAIN      175    198       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    199    219       6 (POTENTIAL).
FT   DOMAIN      220    225       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    226    246       7 (POTENTIAL).
FT   NON_TER     246    246
SQ   SEQUENCE   246 AA;  28430 MW;  8B8F96F8A62E4474 CRC64;
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  Query Match             10.7%;  Score 75.5;  DB 1;  Length 246;
  Best Local Similarity   27.1%;  Pred. No. 2.9;
  Matches   32;  Conservative   18;  Mismatches   47;  Indels   21;  Gaps    5;

Qy         17 VYSVSVGMHNLLLLEGRSWQEMDGQKKH---WKDKVVDLLYWRDIKKTGVVFGASLFLLL 73
              :||  :    :|::   ||  ::    |   |    : : |:  |      |  |:|| |
Db         40 LYSALMTTRKVLIIFNNSWTVIN----HFNIWLATCLSIFYFLMIAN----FSNSIFLSL 91

Qy         74 SLTVFSIVSVTAYIALALLSV---------TISFRIYKGVIQAIAKSDEG-HPFRAYL 121
                | ::|||| ::| || |          ||  :||      : ||   |  | :|
Db         92 RWRVKTVVSVTLLMSLLLLFVNVLVINTFIVISVDVYKVNTSYSSHSDNNIHISRIFL 149


RESULT 13
G6PI_HELPY
ID   G6PI_HELPY     STANDARD;      PRT;   545 AA.
AC   O25781;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
e    DT   28-FEB-2003 (Rel.        1, afmeLatd0fXQpdate)
DE   Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE   isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN   PGI OR HP1166.
OS   Helicobacter pylori (Campylobacter pylori).
OC   Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC   Helicobacteraceae; Helicobacter.
OX   NCBI_TaxID=210;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=26695 / ATCC 700392;
RX   MEDLINE=97394467; PubMed=9252185;
RA   Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA   Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA   Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA   Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA   McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA   Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA   Cotton M.D., Weidman J.M.L.;00XB C., Bowman C., Watthey L., Wallin E.,
RA   Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA   Venter J.C.;
RT   "The complete genome sequence of the gastric pathogen Helicobacter
RT   pylori.";
RL   Nature 388:539-547(1997).
CC   -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC       phosphate.
CC   -!- PATHWAY: Involved in glycolysis and in gluconeogenesis.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
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DR   EMBL; AE000622; AAD08211.1; -.
DR   PIR; F64665; F64665.
DR   HSSP; Q9N1E2; 1HOX.
DR   TIGR; HP1166; -.
DR   HAMAP; MF_00473; -; 1.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR   PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW   Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT   ACT_SITE    382    382       BY SIMILARITY.
FT   ACT_SITE    510    510       BY SIMILARITY.
SQ   SEQUENCE   545 AA;  62487 MW;  BDC68D1625190236 CRC64;

  Query Match             10.7%;  Score 75.5;  DB 1;  Length 545;
  Best Local Similarity   25.3%;  Pred. No. 6.7;
  Matches   37;  Conservative   20;  Mismatches   44;  Indels   45;  Gaps    6;

Qy         23 GMHNLL----------LLEGRSWQEMDGQ---KKHWKDKVVDLLYWRDIKKTGVVFGASL 69
              | | :|           ::|:|::|  |:   |   ||:  || : |      | ||
Db        411 GHHEILFSNVLAQAQAFMKGKSYEEALGELLFKGLDKDEAKDLAHHR------VFFGNRP 464

Qy         70 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSD---------------- 112
                :| |   |  :: | :||    | :     :|||  |   |
Db        465 SNILLLEKISPSNIGALVALYEHKVFV-----QGVIWDINSFDQWGVELGKELAVPILQE 519

Qy        113 -EGHPFRAYLESEVAISEELVQKYSN 137
               |||   || :|    :: |:: | |
Db        520 LEGHKSNAYFDSS---TKHLIELYKN 542


RESULT 14
G6PI_HELPJ
ID   G6PI_HELPJ     STANDARD;      PRT;   545 AA.
AC   Q9ZK49;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE   isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN   PGI OR JHP1093.
OS   Helicobacter pylori J99 (Campylobacter pylori J99).
OC   Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC   Helicobacteraceae; Helicobacter.
OX   NCBI_TaxID=85963;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99120557; PubMed=9923682;
RA   Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA   Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA   Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA   Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA   Trust T.J.;
RT   "Genomic sequence comparison of two unrelated isolates of the human
RT   gastric pathogen Helicobacter pylori.";
RL   Nature 397:176-180(1999).
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CC   -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC       phosphate.
CC   -!- PATHWAY: Involved in glycolysis and in gluconeogenesis.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE001536; AAD06664.1; -.
DR   PIR; E71851; E71851.
DR   HSSP; Q9N1E2; 1HOX.
DR   HAMAP; MF_00473; -; 1.
DR   InterPro; IPR001672; G6P_Isomerase.
DR   Pfam; PF00342; PGI; 1.
DR   PRINTS; PR00662; G6PISOMERASE.
DR   PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR   PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW   Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT   ACT_SITE    382    382       BY SIMILARITY.
FT   ACT_SITE    510    510       BY SIMILARITY.
SQ   SEQUENCE   545 AA;  62302 MW;  7DB544D95FD1D237 CRC64;

  Query Match             10.6%;  Score 74.5;  DB 1;  Length 545;
  Best Local Similarity   25.3%;  Pred. No. 8.4;
  Matches   37;  Conservative   19;  Mismatches   45;  Indels   45;  Gaps    6;

Qy         23 GMHNLL----------LLEGRSWQEMDGQ---KKHWKDKVVDLLYWRDIKKTGVVFGASL 69
              | | :|           ::|:|::|  |:   |   ||:  || : |      | ||
Db        411 GHHEILFSNVLAQAQAFMKGKSYEEALGELLSKGLDKDEAKDLAHHR------VFFGNRP 464

Qy         70 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSD---------------- 112
                :| |   |  :: | :||    | :     :|||  |   |
Db        465 SNILLLEKISPSNIGALVALYEHKVFV-----QGVIWDINSFDQWGVELGKELAVPILQE 519

Qy        113 -EGHPFRAYLESEVAISEELVQKYSN 137
               |||   || :|    :  |:: | |
Db        520 LEGHKSNAYFDSS---TRHLIELYKN 542


RESULT 15
YC73_HAEIN
ID   YC73_HAEIN     STANDARD;      PRT;   268 AA.
AC   P44150;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hypothetical protein HI1273.
GN   HI1273.
OS   Haemophilus influenzae.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC   Pasteurellaceae; Haemophilus.
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OX   NCBI_TaxID=727;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Rd / KW20 / ATCC 51907;
RX   MEDLINE=95350630; PubMed=7542800;
RA   Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA   Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA   McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA   Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA   Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA   Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA   Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA   Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA   Venter J.C.;
RT   "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT   Rd.";
RL   Science 269:496-512(1995).
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CC   -----------------------------------------------------------------------
DR   EMBL; U32807; AAC22921.1; -.
DR   PIR; F64024; F64024.
DR   TIGR; HI1273; -.
DR   InterPro; IPR000051; SAM_bind.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   268 AA;  30510 MW;  E5B28DA7AADC4D0B CRC64;

  Query Match             10.5%;  Score 74;  DB 1;  Length 268;
  Best Local Similarity   25.2%;  Pred. No. 4.4;
  Matches   29;  Conservative   15;  Mismatches   49;  Indels   22;  Gaps    4;

Qy          8 VSCLRENFAVYSVSVGMHNLLLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKTGVVFGA 67
              : ||    | :    |:|:|               | | |       | |: :  ||  :
Db         94 LDCL----AQFKQKFGLHHLTTFH----------KSWADN------WDDVPQADVVLAS 132

Qy         68 SLFLLLSL-TVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSDEGHPFRAYL 121
                 |:  |  :   :   |   : | |||    : :|| :|| : | | |   ||
Db        133 RSTLVDDLDDMIEKLCAKAKKRVFLTSVTQRHFLDEGVFEAIGREDIGFPTYIYL 187


Search completed: January 22, 2004, 16:32:01
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